



SEARCHED LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ANDERTON, STEPHEN MARK
VAN DER ZEE, RUURD
VAN EDEN, WILLEM

(ii) TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: THE WEBB LAW FIRM
(B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
(C) CITY: PITTSBURGH
(D) STATE: PENNSYLVANIA
(E) COUNTRY: UNITED STATES OF AMERICA
(F) ZIP: 15219-1818

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" FLOPPY DISK
(B) COMPUTER: DIGITAL VENTURIS GL 6200
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: MICROSOFT WORD 2.0C

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/716,169
(B) FILING DATE: 18-SEP-1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/NL95/00108
(B) FILING DATE: 21-MAR-1995

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu
1 5 10 15

Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu
20 25 30

Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala
35 40 45

Pro Thr Ile Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu
50 55 60

Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu
65 70 75

Val Ala Lys Lys Thr Asp Asp Val Ala Gly Asp Gly Thr Thr Thr
80 85 90

Ala Thr Val Leu Ala Gln Ala Leu Val Arg Glu Gly Leu Arg Asn
95 100 105

Val Ala Ala Gly Ala Asn Pro Leu Gly Val Lys Arg Gly Ile Glu
110 115 120

Lys Ala Val Glu Lys Val Thr Glu Thr Leu Leu Lys Gly Ala Lys
125 130 135

Glu Val Glu Thr Lys Glu Gln Ile Ala Ala Thr Ala Ala Ile Ser
140 145 150

Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp
155 160 165

Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu Glu Ser Asn Thr
170 175 180

Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg Phe Asp Lys
185 190 195

Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Pro Glu Arg Gln Glu
200 205 210

Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys Val
215 220 225

Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gly
230 235 240

Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu
245 250 255

Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys
260 265 270

Ser Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala
275 280 285

Met Leu Gln Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser
290 295 300

Glu Glu Val Gly Leu Thr Leu Glu Asn Ala Asp Leu Ser Leu Leu
305 310 315

Gly Lys Ala Arg Lys Val Val Val Thr Lys Asp Glu Thr Thr Ile
320 325 330

Val Glu Gly Ala Gly Asp Thr Asp Ala Ile Ala Gly Arg Val Ala
335 340 345

Gln Ile Arg Gln Glu Ile Glu Asn Ser Asp Ser Asp Tyr Asp Arg
 350 355 360
 Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala
 365 370 375
 Val Ile Lys Ala Gly Ala Ala Thr Glu Val Glu Leu Lys Glu Arg
 380 385 390
 Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala Lys Ala Ala Val
 395 400 405
 Glu Glu Gly Ile Val Ala Gly Gly Val Thr Leu Leu Gln Ala
 410 415 420
 Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp Glu Ala Thr
 425 430 435
 Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu Lys Gln
 440 445 450
 Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu Lys
 455 460 465
 Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly
 470 475 480
 Val Lys Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys
 485 490 495
 Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu
 500 505 510
 Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu
 515 520 525
 Lys Ala Ser Val Pro Gly Gly Asp Met Gly Gly Met Asp Phe
 530 535 540

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
 1 5 10 15

Val Phe Arg Ala Ala Leu Lys Asn Pro Asp Ile Glu Val Val Ala
 20 25 30

Val Asn Asp Leu Thr Asp Ala Asn Thr Leu Ala His Leu Leu Lys
35 40 45
Tyr Asp Ser Val His Gly Arg Leu Asp Ala Glu Val Ser Val Asn
50 55 60
Gly Asn Asn Leu Val Val Asn Gly Lys Glu Ile Ile Val Lys Ala
65 70 75
Glu Arg Asp Pro Glu Asn Leu Ala Trp Gly Glu Ile Gly Val Asp
80 85 90
Ile Val Val Glu Ser Thr Gly Arg Phe Thr Lys Arg Glu Asp Ala
95 100 105
Ala Lys His Leu Glu Ala Gly Ala Lys Lys Val Ile Ile Ser Ala
110 115 120
Pro Ala Lys Asn Glu Asp Ile Thr Ile Val Met Gly Val Asn Gln
125 130 135
Asp Lys Tyr Asp Pro Lys Ala His His Val Ile Ser Asn Ala Ser
140 145 150
Cys Thr Thr Asn Cys Leu Ala Pro Phe Ala Lys Val Leu His Glu
155 160 165
Gln Phe Gly Ile Val Arg Gly Met Met Thr Thr Val His Ser Tyr
170 175 180
Thr Asn Asp Gln Arg Ile Leu Asp Leu Pro His Lys Asp Leu Arg
185 190 195
Arg Ala Arg Ala Ala Ala Glu Ser Ile Ile Pro Thr Thr Thr Gly
200 205 210
Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys
215 220 225
Leu Asn Gly Met Ala Met Arg Val Pro Thr Pro Asn Val Ser Val
230 235 240
Val Asp Leu Val Ala Glu Leu Glu Lys Glu Val Thr Val Glu Glu
245 250 255
Val Asn Ala Ala Leu Lys Ala Ala Ala Glu Gly Glu Leu Lys Gly
260 265 270
Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn
275 280 285

Gly Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val
290 295 300

Ile Asp Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu
305 310 315

Thr Gly Tyr Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala
320 325 330

Ser Lys Gly

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val
1 5 10 15

Thr Arg Ala Ala Phe Ser Cys Asp Lys Val Asp Ile Val Ala Ile
20 25 30

Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
35 40 45

Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu
50 55 60

Asn Gly Lys Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln
65 70 75

Glu Arg Asp Pro Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu
80 85 90

Tyr Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala
95 100 105

Gly Ala His Leu Lys Gly Gly Ala Lys Arg Val Ile Ile Ser Ala
110 115 120

Pro Ser Ala Asp Ala Pro Met Phe Val Met Gly Val Asn His Glu
125 130 135

Lys Tyr Asp Asn Ser Leu Lys Ile Val Ser Asn Ala Ser Cys Thr
140 145 150

Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp Asn Phe
155 160 165

Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala Ile Thr Ala
 170 175 180
 Thr Gln Lys Thr Val Asp Gly Pro Ser Gly Lys Leu Trp Arg Asp
 185 190 195
 Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ala Ser Thr Gly Ala
 200 205 210
 Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly Lys Leu
 215 220 225
 Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val Ser Val Val
 230 235 240
 Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile
 245 250 255
 Lys Lys Val Val Lys Gln Ala Ala Glu Gly Pro Leu Lys Gly Ile
 260 265 270
 Leu Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser
 275 280 285
 Asn Ser His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu
 290 295 300
 Asn Asp Asn Ile Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr
 305 310 315
 Gly Tyr Ser Asn Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser
 320 325 330

Lys Glu

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTON: SEQ ID NO: 4:

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser
 1 5 10 15

Arg Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val
 20 25 30

Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp
 35 40 45

Leu Leu Ala Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg
 50 55 60
 Thr Val Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys
 65 70 75
 Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr
 80 85 90
 Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr
 95 100 105
 Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
 110 115 120
 Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala
 125 130 135
 Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala
 140 145 150
 Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro
 155 160 165
 Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys
 170 175 180
 Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg
 185 190 195
 Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu
 200 205 210
 Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser
 215 220 225
 Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
 230 235 240
 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln
 245 250 255
 Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro
 260 265 270
 Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr
 275 280 285
 Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val
 290 295 300

Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp
 305 310 315
 Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu
 320 325 330
 Thr Leu Asn Leu Glu Asp Val Gln Pro His Asp Leu Gly Lys Val
 335 340 345
 Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met Leu Leu Lys Gly
 350 355 360
 Lys Gly Asp Lys Ala Gln Ile Glu Lys Arg Ile Gln Glu Ile Ile
 365 370 375
 Glu Gln Leu Asp Val Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu
 380 385 390
 Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys
 395 400 405
 Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg
 410 415 420
 Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly
 425 430 435
 Ile Val Leu Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala
 440 445 450
 Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile
 455 460 465
 Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
 470 475 480
 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met
 485 490 495
 Gln Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe
 500 505 510
 Val Asn Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val
 515 520 525
 Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr
 530 535 540
 Thr Ala Glu Val Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp
 545 550 555

Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly
560 565 570

Gly Met Phe

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 547

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ala Lys Asp Val Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu
1 5 10 15

Gln Gly Val Asp Leu Leu Ala Asp Ala Val Ala Val Thr Met Gly
20 25 30

Pro Lys Gly Arg Thr Val Ile Ile Glu Gln Ser Trp Gly Ser Pro
35 40 45

Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu
50 55 60

Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val
65 70 75

Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Ala
80 85 90

Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile
95 100 105

Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu
110 115 120

Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro
125 130 135

Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
140 145 150

Asn Gly Asp Lys Asp Ile Gly Asn Ile Ile Ser Asp Ala Met Lys
155 160 165

Lys Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr
170 175 180

Leu Asn Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg
185 190 195

Gly Tyr Ile Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys
 200 205 210
 Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile
 215 220 225
 Ser Ser Val Gln Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala
 230 235 240
 His Arg Lys Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu
 245 250 255
 Ala Leu Ser Thr Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln
 260 265 270
 Val Val Ala Val Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn
 275 280 285
 Gln Leu Lys Asp Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly
 290 295 300
 Glu Glu Gly Leu Asn Leu Asn Leu Glu Asp Val Gln Ala His Asp
 305 310 315
 Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met
 320 325 330
 Leu Leu Lys Gly Lys Gly Asp Lys Ala His Ile Glu Lys Arg Ile
 335 340 345
 Gln Glu Ile Thr Glu Gln Leu Asp Ile Thr Thr Ser Glu Tyr Glu
 350 355 360
 Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val
 365 370 375
 Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
 380 385 390
 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala
 395 400 405
 Val Glu Glu Gly Ile Val Leu Gly Gly Cys Ala Leu Leu Arg
 410 415 420
 Cys Ile Pro Ala Leu Asp Ser Leu Lys Pro Ala Asn Glu Asp Gln
 425 430 435
 Lys Ile Gly Ile Glu Ile Ile Lys Arg Ala Leu Lys Ile Pro Ala
 440 445 450

Met Thr Ile Ala Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val
 455 460 465
 Glu Lys Ile Leu Gln Ser Ser Ser Glu Val Gly Tyr Asp Ala Met
 470 475 480
 Leu Gly Asp Phe Val Asn Met Val Glu Lys Gly Ile Ile Asp Pro
 485 490 495
 Thr Lys Val Val Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala
 500 505 510
 Ser Leu Leu Thr Thr Ala Glu Ala Val Val Thr Glu Ile Pro Lys
 515 520 525
 Glu Glu Lys Asp Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly
 530 535 540
 Gly Met Gly Gly Gly Met Phe
 545

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 555
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly
 1 5 10 15
 Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
 20 25 30
 Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile
 35 40 45
 Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val
 50 55 60
 Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile
 65 70 75
 Gly Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu
 80 85 90
 Ala Gly Asp Gly Thr Thr Ala Thr Val Leu Ala Arg Ser Ile
 95 100 105
 Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala Asn Pro Val
 110 115 120

Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala Val Ile Ala
 125 130 135
 Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro Glu Glu Ile
 140 145 150
 Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys Asp Ile Gly
 155 160 165
 Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg Lys Gly Val
 170 175 180
 Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu Leu Glu Ile
 185 190 195
 Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe
 200 205 210
 Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln Asp Ala Tyr
 215 220 225
 Val Leu Leu Ser Glu Lys Lys Phe Ser Ser Val Gln Ser Ile Val
 230 235 240
 Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val Ile
 245 250 255
 Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
 260 265 270
 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro
 275 280 285
 Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile
 290 295 300
 Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Asn Leu Asn
 305 310 315
 Leu Glu Asp Val Gln Ala His Asp Leu Gly Lys Val Gly Glu Val
 320 325 330
 Ile Val Thr Lys Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp
 335 340 345
 Lys Ala His Ile Glu Lys Arg Ile Gln Glu Ile Thr Glu Gln Leu
 350 355 360
 Asp Ile Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu Asn Glu Arg
 365 370 375

Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys Val Gly Gly
380 385 390

Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg Val Thr Asp
395 400 405

Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Leu
410 415 420

Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala Leu Asp Ser
425 430 435

Leu Lys Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile Glu Ile Ile
440 445 450

Lys Arg Ala Leu Lys Ile Pro Ala Met Thr Ile Ala Lys Asn Ala
455 460 465

Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Leu Gln Ser Ser
470 475 480

Ser Glu Val Gly Tyr Asp Ala Met Leu Gly Asp Phe Val Asn Met
485 490 495

Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
500 505 510

Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu
515 520 525

Ala Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met
530 535 540

Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
545 550 555